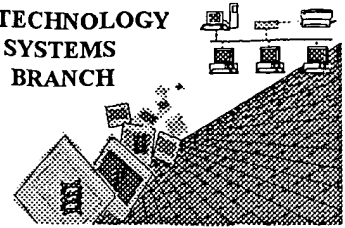


no location

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/609,383
Source: O/P/E
Date Processed by STIC: 7/28/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/efb/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 16/609,383

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 3rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING

DATE: 07/28/2003

PATENT APPLICATION: US/10/609,383

TIME: 15:34:59

Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\07282003\J609383.raw

insert

1 <110> APPLICANT: Feldmann, Richard J.; Connectron Holding, Inc.
 3 <120> TITLE OF INVENTION: Synthetic Connectron
 5 <130> FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 E--> 7 <140> CURRENT APPLICATION NUMBER: US/10/609,383
 C--> 7 <141> CURRENT FILING DATE: 2003-07-01
 8 <150> PRIOR APPLICATION NUMBER: US 60/393,558 and US 09/866,925
 10 <160> NUMBER OF SEQ ID NOS: 29
 12 <170> SOFTWARE: Proprietary

list separately, with separate <150> and <151> lines

*<151> 72002-07-05
 -> 09/866,925
 -> 72001-05-30*

ERRORED SEQUENCES

Does Not Comply
 Corrected Diskette Needed

see p. 2 for more errors

2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/609,383

DATE: 07/31/2003

TIME: 13:32:30

Input Set : N:\AMC\609383.txt

Output Set: N:\CRF4\07312003\J609383.raw

300 <210> SEQ ID NO: 18
302 <211> LENGTH: 194
303 <212> TYPE: DNA
304 <213> ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
306 <220> FEATURE:
307 <222> LOCATION: (4836528)...(4836720)
308 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =

53531

311 <400> SEQUENCE: 18
312 ggacggcaaa caggtggtcg agcagaccat ccgcgcgatg aacgagcttt ccgagaagat 60
313 cagcgccctcc tgcgccaaca tcgaggccct caacagccgc acggtgaaca tcggccagat 120
314 cctcgaagtg atcaagggca tctccgagca gaccaacctg ctgcgcctca acgccgcat 180
315 cgaagccgcg cgcg 194

318 <210> SEQ ID NO: 19
320 <211> LENGTH: 169
321 <212> TYPE: DNA
322 <213> ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
324 <220> FEATURE:
325 <222> LOCATION: (4838678)...(4838846)
326 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =

53549a

329 <400> SEQUENCE: 19
330 accatccgcg cgatgaacga gctttccgag aagatcagcg cctcctgcgc caacatcgag 60
331 gccctcaaca gccgcacggt gaacatcggc cagatcctcg aagtgatcaa gggcatctcc 120
332 gaggagacca acctgctcgc cctcaacgcc gccatcgaag ccgcgcgcg 169

335 <210> SEQ ID NO: 20
337 <211> LENGTH: 36
338 <212> TYPE: DNA
339 <213> ORGANISM: Sequence Recognized by Synthetic DNA Binding Protein

341 <220> FEATURE:
344 <400> SEQUENCE: 20
345 tccccatgag catagatatg caggtaggcg gcaagt
348 <210> SEQ ID NO: 21
350 <211> LENGTH: 136
351 <212> TYPE: DNA
352 <213> ORGANISM: Vibrio cholerae chromosome I, complete chromosome.
354 <220> FEATURE:
355 <222> LOCATION: (952641)...(952777)
356 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =

607

359 <400> SEQUENCE: 21
360 tgtatataacc caaactactt ggagttgcag gtaggcggca agtgagtgag tccccatgag 60
361 catagataga ctatgtgatt ggggtgaacg aacgtagcca acaccgctgc agcttcaagt 120
362 aggaagggta tacctt 136

365 <210> SEQ ID NO: 22
367 <211> LENGTH: 117
368 <212> TYPE: DNA
369 <213> ORGANISM: Vibrio cholerae chromosome I, complete chromosome.
371 <220> FEATURE:
372 <222> LOCATION: (1005810)...(1005926)
373 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =

646

376 <400> SEQUENCE: 22

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/609,383

DATE: 07/28/2003
TIME: 15:35:00

Input Set : N:\DA\pto.da.txt
Output Set: N:\CRF4\07282003\J609383.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 27,28,29,30
Seq#:2; Line(s) 45,46,47,48
Seq#:3; Line(s) 63,64,65
Seq#:4; Line(s) 76,80
Seq#:5; Line(s) 95
Seq#:6; Line(s) 110
Seq#:7; Line(s) 121,125
Seq#:8; Line(s) 140
Seq#:9; Line(s) 155
Seq#:10; Line(s) 170
Seq#:12; Line(s) 200,201,202,203,204,205,206,207,208
Seq#:13; Line(s) 222,223,224
Seq#:14; Line(s) 238,239,240
Seq#:15; Line(s) 255,256,257,258
Seq#:16; Line(s) 273,274
Seq#:17; Line(s) 289,290,291
Seq#:18; Line(s) 306,307,308,309
Seq#:19; Line(s) 324,325,326
Seq#:20; Line(s) 339
Seq#:21; Line(s) 354,355,356
Seq#:22; Line(s) 371,372
Seq#:23; Line(s) 385
Seq#:24; Line(s) 400,401,402
Seq#:25; Line(s) 417,418
Seq#:26; Line(s) 432
Seq#:27; Line(s) 446
Seq#:28; Line(s) 461,462
Seq#:29; Line(s) 477,478,479

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/609,383

DATE: 07/28/2003

TIME: 15:35:00

Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\07282003\J609383.raw

L:7 M:282 E: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.

L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:426 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:

L:440 M:259 W: Allowed number of lines exceeded, <213> ORGANISM: